

SEQUENCE LISTING

<110> STRYKER CORPORATION

<120> REPAIR OF LARYNX, TRACHEA, AND OTHER FIBROCARTILAGINOUS TISSUES

<130> STK-070 PCT

<140> PCT/US99/17222

<141> 1999-07-30

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1822

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(1341)

<400> 1

ggtgccggcc	cgagccccgg	agcccccgtta	gcgcgttagag	ccggcgcg	atg	cac	gtg	57
					Met	His	Val	
								1

cgc	tca	ctg	cga	gct	gct	gct	gct	105
Arg	Ser	Leu	Arg	Ala	Ala	Pro	His	
5	10	15						

ccc	ctg	ttc	ctg	ctg	cgc	tcc	gcc	gac	ttc	agc	ctg	gac	aac	153
Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	Leu	Asp
20	25		30		35									

gag	gtg	cac	tcg	agc	ttc	atc	cac	cg	ctc	cgc	agc	cag	gag	cg	201
Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	
40		45													

cg	gag	atg	cag	cgc	gag	atc	ctc	tcc	att	ttg	ggc	ttg	ccc	cac	cgc	249
Arg	Glu	Met	Gln	Arg	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg		
55		60														

ccg	cgc	ccg	cac	ctc	cag	ggc	aag	cac	aac	tcg	gca	ccc	atg	ttc	atg	297
Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	
70		75														

ctg	gac	ctg	tac	aac	gcc	atg	gct	gtg	gag	gag	ggc	ggc	ggc	ccc	ggc	345
Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly	
85		90														

ggc	cag	ggc	ttc	tcc	tac	ccc	tac	aag	gcc	gtc	ttc	agt	acc	cag	ggc	393
Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
100		105														

Sequence Listing

ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac		441	
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp			
120	125	130	
atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc		489	
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe			
135	140	145	
cac cca cgc tac cac cat cga gag ttc cggttt gat ctt tcc aag atc		537	
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile			
150	155	160	
cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cggtt ac tac aag gac		585	
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp			
165	170	175	
tac atc cggtttt gaa cgc ttc gac aat gag acg ttc cggtt ac tac aag gac		633	
Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr			
180	185	190	195
cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc		681	
Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu			
200	205	210	
gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac		729	
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp			
215	220	225	
atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cggtttt cac aac ctg		777	
Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu			
230	235	240	
ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc		825	
Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro			
245	250	255	
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc		873	
Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro			
260	265	270	275
ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cggtttt agc atc		921	
Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile			
280	285	290	
cggtttt acg ggg agc aaa cag cgc agc cag aac ccgtttt tcc aag acg ccc		969	
Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro			
295	300	305	
aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc		1017	
Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser			
310	315	320	
agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc		1065	
Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe			
325	330	335	

cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340	345	350	355	1113
gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360	365		370	1161
aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375	380		385	1209
ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390	395		400	1257
atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405	410		415	1305
tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420	425		430	1351
 G S E R E S D N D S D H D G E S D T				
gagaattcag accctttggg gccaagttt tctggatcct ccattgctcg ccttggccag 1411				
gaaccagcag accaactgcc ttttgtgaga cttcccccctc cctatccccca actttaaagg 1471				
tgtgagagta ttaggaaaca tgagcagcat atggctttt atcagttttt cagtggcagc 1531				
atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcagggaaa aaaaaacaac 1591				
gcataaagaa aaatggccgg gccaggtcat tggctggaa gtctcagcca tgcacggact 1651				
cgttccaga ggtaattatg agcgcctacc agccaggcca cccagccgtg ggaggaaggg 1711				
ggcgtggcaa ggggtggca cattggtgta tgcgaaaag gaaaattgac ccggaagtcc 1771				
ctgtaataaa tgtcacaata aaacgaatga ataaaaaaaaaaaaaaa a				1822

<210> 2
<211> 431
<212> PRT
<213> Homo sapiens

<400> 2				
Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala	1	5	10	15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser	20	25		30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser	35	40		45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu	50	55	60	

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

<210> 3
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: OPX

<220>
<223> each Xaa is independently selected from a group of one
or more specified amino acids as defined in the
specification.

<400> 3
Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
 1 5 10 15

Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 20 25 30

Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 50 55 60

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 65 70 75 80

Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
 85 90 95

Xaa Ala Cys Gly Cys His
 100

<210> 4
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Generic-Seq-7

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 4

Leu	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10							15

Pro	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Pro
					20			25				30			

Xaa	Asn	His	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa						
							35		40			45			

Xaa	Cys	Cys	Xaa	Pro											
							50		55			60			

Xaa															
							65		70			75			80

Val	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa	Xaa	Cys	Xaa	Cys
							85		90			95			

Xaa

<210> 5

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Generic-Seq-8

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 5

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Trp	Xaa
1					5				10						15

Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Tyr	Cys	Xaa	Gly
					20			25				30			

Xaa	Cys	Xaa	Xaa	Pro	Xaa										
							35		40			45			

Xaa															
							50		55			60			

Xaa	Cys	Cys	Xaa	Pro	Xaa										
							65		70			75			80

0987654321

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
85 90 95

Xaa Xaa Cys Xaa Cys Xaa
100

```
<210> 6
<211> 97
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Generic-Seq-9

<220>
<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
65 70 75 80

xaa

```
<210> 7
<211> 102
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Generic-Seq-10

<220>
<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

```

<400> 7
Cys Xaa Xaa
    1           5           10          15

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly
    20          25          30

Xaa Cys Xaa Xaa
    35          40          45

Xaa Xaa
    50          55          60

Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
    65          70          75          80

Xaa Xaa
    85          90          95

Xaa Xaa Cys Xaa Cys Xaa
    100

```

DRAFT DRAFT DRAFT DRAFT DRAFT

```

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative sequence

<220>
<223> each Xaa is independently selected from a group of one
      or more specified amino acids as defined in the
      specification.

<400> 8
Cys Xaa Xaa Xaa Xaa
    1           5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative sequence

<220>
<223> each Xaa is independently selected from a group of one
      or more specified amino acids as defined in the
      specification.

<400> 9
Cys Xaa Xaa Xaa Xaa
    1           5

```